

# SEQUENCE LISTING

<110> Reed, John C.  
Takayama, Shinichi

<120> Novel BAG Proteins and Nucleic Acid Molecules Encoding Them

<130> P-LJ 3737

<140> 09/394,142

<141> 1999-09-09

<150> 09/150,489

<151> 1998-09-09

<160> 24

<170> PatentIn Ver. 2.0

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Ile Gln Gln Gly Phe Leu Pro Lys Asp Leu Gln Ala Glu Ala Leu Cys  
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Lys Leu Asp Arg Arg Val Lys Ala Thr Ile Glu Gln Phe Met Lys Ile  
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Leu Glu Glu Ile Asp Thr Leu Ile Leu Pro Glu Asn Phe Lys Asp Ser  
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Val Glu Gln Glu Lys Glu Ile Leu Leu Glu Met Ile His Ser Ile Gln

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 Asp Gln Lys Phe Leu Ala Gly Gln Leu Leu Pro Pro Phe Ile Ser Ser  
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 Gly Arg Pro Gln Pro Ser Met Ser Ala Ala Thr His Ser Pro Met Met  
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Arg Gly Tyr Ile Ser Ile Pro Val Ile His Glu Gln Asn Val Thr Arg				
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Ala Gln Arg Gly Glu Tyr Gln Thr His Gln Pro Val Tyr His Lys Ile				

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Ser Ser Thr Pro Leu His Ser Pro Ser Pro Ile Arg Val His Thr Val			
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Val Asp Arg Pro Gln Gln Pro Met Thr His Arg Glu Thr Ala Pro Val			
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Glu Leu Pro Pro Gly His Ile Pro Ile Gln Val Ile Arg Lys Glu Val			
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Gly Pro Ser Ala Val Pro Ser Ser Pro Lys Ser Val Ala Thr Glu Glu			
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Gly Glu Ala Glu Ala Pro Pro Lys His Pro Gly Val Leu Lys Val Glu			
515	520	525	
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Leu Glu Lys Leu Glu Gln Lys Ala Ile Asp Val Pro Gly Gln Val Gln			
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Val Tyr Glu Leu Gln Pro Ser Asn Leu Glu Ala Asp Gln Pro Leu Gln			
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Ala Gly Asn Ala Glu Asp Pro His Thr Glu Thr Gln Gln Pro Glu Ala			
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Thr Ala Ala Ala Thr Ser Asn Pro Ser Ser Met Thr Asp Thr Pro Gly			
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Asn Pro Ala Ala Pro			
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 50 55 60  
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 115 120 125  
 Glu Ile Lys Ile Asp Pro Gln Thr Gly Trp Pro Phe Phe Val Asp His  
 130 135 140  
 Asn Ser Arg Thr Thr Thr Trp Asn Asp Pro Arg Val Pro Ser Glu Gly  
 145 150 155 160  
 Pro Lys Glu Thr Pro Ser Ser Ala Asn Gly Pro Ser Arg Glu Gly Ser  
 165 170 175  
 Arg Leu Pro Pro Ala Arg Glu Gly His Pro Val Tyr Pro Gln Leu Arg  
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Pro Gly Tyr Ile Pro Ile Pro Val Leu His Glu Gly Ala Glu Asn Arg  
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Gln Val His Pro Phe His Val Tyr Pro Gln Pro Gly Met Gln Arg Phe  
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Arg Thr Glu Ala Ala Ala Ala Ala Pro Gln Arg Ser Gln Ser Pro Leu  
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Arg Gly Met Pro Glu Thr Thr Gln Pro Asp Lys Gln Cys Gly Gln Val  
 245 250 255

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Ser Gln Ser Pro Ala Ala Ser Asp Cys Ser Ser Ser Ser Ser Ser Ala  
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Pro Ala Ala Gln Pro Ser Phe His Lys Ala Gln Lys Thr His Tyr Pro  
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Gln Gly Asp Asp Trp Glu Pro Arg Pro Leu Arg Ala Ala Ser Pro Phe  
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Arg Ala Ala Pro Ser Thr Ala Pro Ala Glu Ala Thr Pro Pro Lys Pro  
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Gly Glu Ala Glu Ala Pro Pro Lys His Pro Gly Val Leu Lys Val Glu  
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Ala Ile Leu Glu Lys Val Gln Gly Leu Glu Gln Ala Val Asp Asn Phe  
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Glu Gly Lys Lys Thr Asp Lys Lys Tyr Leu Met Ile Glu Glu Tyr Leu  
 545 550 555 560

Thr Lys Glu Leu Leu Ala Leu Asp Ser Val Asp Pro Glu Gly Arg Ala  
 565 570 575

Asp Val Arg Gln Ala Arg Arg Asp Gly Val Arg Lys Val Gln Thr Ile  
 580 585 590

Leu Glu Lys Leu Glu Gln Lys Ala Ile Asp Val Pro Gly Gln Val Gln  
 595 600 605

Val Tyr Glu Leu Gln Pro Ser Asn Leu Glu Ala Asp Gln Pro Leu Gln  
 610 615 620

Ala Ile Met Glu Met Gly Ala Val Ala Ala Asp Lys Gly Lys Lys Asn  
 625 630 635 640

Ala Gly Asn Ala Glu Asp Pro His Thr Glu Thr Gln Gln Pro Glu Ala  
 645 650 655

Thr Ala Ala Ala Thr Ser Asn Pro Ser Ser Met Thr Asp Thr Pro Gly  
 660 665 670

Asn Pro Ala Ala Pro  
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<211> 1010

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (323)..(1009)

<400> 7

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cgtatgggtcc aacatacccc ccaggccctg gggcaaatac tgcctcatac tcaggggctt 120
attatgcacc tggttatact cagaccagtt actccacaga agttccaagt acttaccgtt 180
catctggcaa cagcccaact ccagtctctc gttggatcta tccccagcag gactgtcaag 240
actgaagcac cccctcttaa ggggcaggtt ccaggatata cgccttcaca gaaccctgga 300
atgaccctgc cccattatcc tt atg gag atg gta atc gta gtg ttc cac aat 352
                        Met Glu Met Val Ile Val Val Phe His Asn
                        1             5             10
cac ggc cga ctg tac gac cac aag aaa gat gcg tgg gct tct cct ggt 400
His Gly Arg Leu Tyr Asp His Lys Lys Asp Ala Trp Ala Ser Pro Gly
                        15             20             25
gct tat gga atg ggt ggc cgt tat ccc tgg cct tca tca gcg ccc tca 448
Ala Tyr Gly Met Gly Gly Arg Tyr Pro Trp Pro Ser Ser Ala Pro Ser
                        30             35             40
gca cca ccc ggc aat ctc tac atg act gaa agt act tca cca tgg cct 496
Ala Pro Pro Gly Asn Leu Tyr Met Thr Glu Ser Thr Ser Pro Trp Pro
                        45             50             55
agc agt ggc tct ccc cag tca ccc cct tca ccc cca gtc cag cag ccc 544
Ser Ser Gly Ser Pro Gln Ser Pro Pro Ser Pro Pro Val Gln Gln Pro
                        60             65             70
aag gat tct tca tac ccc tat agc caa tca gat caa agc atg aac cgg 592
Lys Asp Ser Ser Tyr Pro Tyr Ser Gln Ser Asp Gln Ser Met Asn Arg
                        75             80             85
cac aac ttt cct tgc agt gtc cat cag tac gaa tcc tcg ggg aca gtg 640
His Asn Phe Pro Cys Ser Val His Gln Tyr Glu Ser Ser Gly Thr Val
                        95             100             105
aac aat gat gat tca gat ctt ttg gat tcc caa gtc cag tat agt gct 688
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Asn Asn Asp Asp Ser Asp Leu Leu Asp Ser Gln Val Gln Tyr Ser Ala	
110 115 120	
gag cct cag ctg tat ggt aat gcc acc agt gac cat ccc aac aat caa	736
Glu Pro Gln Leu Tyr Gly Asn Ala Thr Ser Asp His Pro Asn Asn Gln	
125 130 135	
gat caa agt agc agt ctt cct gaa gaa tgt gta cct tca gat gaa agt	784
Asp Gln Ser Ser Ser Leu Pro Glu Glu Cys Val Pro Ser Asp Glu Ser	
140 145 150	
act cct ccg agt att aaa aaa atc ata cat gtg ctg gag aag gtc cag	832
Thr Pro Pro Ser Ile Lys Lys Ile Ile His Val Leu Glu Lys Val Gln	
155 160 165 170	
tat ctt gaa caa gaa gta gaa gaa ttt gta gga aaa aag aca gac aaa	880
Tyr Leu Glu Gln Glu Val Glu Glu Phe Val Gly Lys Lys Thr Asp Lys	
175 180 185	
gca tac tgg ctt ctg gaa gaa atg cta acc aag gaa ctt ttg gaa ctg	928
Ala Tyr Trp Leu Leu Glu Glu Met Leu Thr Lys Glu Leu Leu Glu Leu	
190 195 200	
gat tca gtt gaa act ggg ggc cag gac tct gta cgg cag gcc aga aaa	976
Asp Ser Val Glu Thr Gly Gly Gln Asp Ser Val Arg Gln Ala Arg Lys	
205 210 215	
gag gct gtt tgt aag att cag gcc ata ttg gaa a	1010
Glu Ala Val Cys Lys Ile Gln Ala Ile Leu Glu	
220 225	

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<211> 229

<212> PRT

<213> Homo sapiens

<400> 8

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His Lys Lys Asp Ala Trp Ala Ser Pro Gly Ala Tyr Gly Met Gly Gly
20 25 30

Arg Tyr Pro Trp Pro Ser Ser Ala Pro Ser Ala Pro Pro Gly Asn Leu
35 40 45

Tyr Met Thr Glu Ser Thr Ser Pro Trp Pro Ser Ser Gly Ser Pro Gln



50	55	60
Ser Pro Pro Ser Pro Pro Val Gln Gln Pro Lys Asp Ser Ser Tyr Pro		
65	70	75 80
Tyr Ser Gln Ser Asp Gln Ser Met Asn Arg His Asn Phe Pro Cys Ser		
	85	90 95
Val His Gln Tyr Glu Ser Ser Gly Thr Val Asn Asn Asp Asp Ser Asp		
	100	105 110
Leu Leu Asp Ser Gln Val Gln Tyr Ser Ala Glu Pro Gln Leu Tyr Gly		
	115	120 125
Asn Ala Thr Ser Asp His Pro Asn Asn Gln Asp Gln Ser Ser Ser Leu		
	130	135 140
Pro Glu Glu Cys Val Pro Ser Asp Glu Ser Thr Pro Pro Ser Ile Lys		
	145	150 155 160
Lys Ile Ile His Val Leu Glu Lys Val Gln Tyr Leu Glu Gln Glu Val		
	165	170 175
Glu Glu Phe Val Gly Lys Lys Thr Asp Lys Ala Tyr Trp Leu Leu Glu		
	180	185 190
Glu Met Leu Thr Lys Glu Leu Leu Glu Leu Asp Ser Val Glu Thr Gly		
	195	200 205
Gly Gln Asp Ser Val Arg Gln Ala Arg Lys Glu Ala Val Cys Lys Ile		
	210	215 220
Gln Ala Ile Leu Glu		
225		

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    1             5             10             15

tac ctg agc tcc aaa aca gaa ttg cag ggt tta att gga cag ttg gat      95
Tyr Leu Ser Ser Lys Thr Glu Leu Gln Gly Leu Ile Gly Gln Leu Asp
          20             25             30

gag gta agt ntt gaa aaa aac ccc tgc atc cgg gaa gcc agg aga aga      143
Glu Val Ser Xaa Glu Lys Asn Pro Cys Ile Arg Glu Ala Arg Arg Arg
          35             40             45

gca gtg atc gag gtg caa act ctg atc aca tat att gac ttg aag gag      191
Ala Val Ile Glu Val Gln Thr Leu Ile Thr Tyr Ile Asp Leu Lys Glu
          50             55             60

gcc ctt gag aaa aga aag ctg ttt gct tgt gag gag cac cca tcc cat      239
Ala Leu Glu Lys Arg Lys Leu Phe Ala Cys Glu Glu His Pro Ser His
          65             70             75

aaa gcc gtc tgg aac gtc ctt gga aac ttg tct gag atc cag gga gaa      287
Lys Ala Val Trp Asn Val Leu Gly Asn Leu Ser Glu Ile Gln Gly Glu
          80             85             90             95

gtt ctt tca ttt gat gga aat cga acc gat aag aac tac atc cgg ctg      335
Val Leu Ser Phe Asp Gly Asn Arg Thr Asp Lys Asn Tyr Ile Arg Leu
          100             105             110

gaa gag ctg ctc acc aag cag ctg cta gcc ctg gat gct gtt gat ccg      383
Glu Glu Leu Leu Thr Lys Gln Leu Leu Ala Leu Asp Ala Val Asp Pro
          115             120             125

cag gga gaa gag aag tgt aag gct gcc agg aaa caa gct gtg agg ctt      431
Gln Gly Glu Glu Lys Cys Lys Ala Ala Arg Lys Gln Ala Val Arg Leu
          130             135             140

gcg cag aat att ctc agc tat ctc gac ctg aaa tct gat gaa tgg gag      479
Ala Gln Asn Ile Leu Ser Tyr Leu Asp Leu Lys Ser Asp Glu Trp Glu
          145             150             155

tac tgaataacca gagatctcac ttttgatact gttttgcact tcatatgtgc      532
Tyr
160

ttctatgtat agagagcttt cagttcattg atttatacgt gcatatttca gtctcagtat 592
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ttatgattga agcaaattct attcagtatc tgctgctttt gatgttgcaa gacaaatata 652

attacagcac gttaactttt ccattcggat caaaaaa 689

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<211> 160

<212> PRT

<213> Homo sapiens

<400> 10

Glu Ile Lys Asn Glu Leu Leu Gln Ala Gln Asn Pro Ser Glu Leu Tyr  
1 5 10 15

Leu Ser Ser Lys Thr Glu Leu Gln Gly Leu Ile Gly Gln Leu Asp Glu  
20 25 30

Val Ser Xaa Glu Lys Asn Pro Cys Ile Arg Glu Ala Arg Arg Arg Ala  
35 40 45

Val Ile Glu Val Gln Thr Leu Ile Thr Tyr Ile Asp Leu Lys Glu Ala  
50 55 60

Leu Glu Lys Arg Lys Leu Phe Ala Cys Glu Glu His Pro Ser His Lys  
65 70 75 80

Ala Val Trp Asn Val Leu Gly Asn Leu Ser Glu Ile Gln Gly Glu Val  
85 90 95

Leu Ser Phe Asp Gly Asn Arg Thr Asp Lys Asn Tyr Ile Arg Leu Glu  
100 105 110

Glu Leu Leu Thr Lys Gln Leu Leu Ala Leu Asp Ala Val Asp Pro Gln  
115 120 125

Gly Glu Glu Lys Cys Lys Ala Ala Arg Lys Gln Ala Val Arg Leu Ala  
130 135 140

Gln Asn Ile Leu Ser Tyr Leu Asp Leu Lys Ser Asp Glu Trp Glu Tyr  
145 150 155 160

<210> 11

<211> 246

<212> DNA

<213> Caenorhabditis elegans

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gacctgcttt gggtttttcga gaaaaccacg ttccaaatca gcgacatctc tcaaattgag 120  
atcataggct ttttgaagat tgctcaaatt atgcttctca tattgcatga gcattttgaa 180  
gcccgcgtca tcaaccaaag cattttttcc acccatcaca atgattttat cattttcttt 240  
aaaatt 246

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<213> Caenorhabditis elegans

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Met Lys Val Asn Val Ser Cys Ser Ser Val Gln Thr Thr Ile Asp Ile  
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20 25 30  
Leu Arg Asp Arg Ile Ala Thr Asp Asn Asp Val Asp Val Glu Thr Met  
35 40 45  
Lys Leu Leu His Arg Gly Lys Phe Leu Gln Gly Ala Asp Asp Val Ser  
50 55 60  
Leu Ser Thr Leu Asn Phe Lys Glu Asn Asp Lys Ile Ile Val Met Gly  
65 70 75 80  
Gly Lys Asn Ala Leu Val Asp Asp Ala Gly Phe Lys Met Leu Met Gln  
85 90 95  
Tyr Glu Lys His Asn Leu Ser Asn Leu Gln Lys Ala Tyr Asp Leu Asn  
100 105 110  
Leu Arg Asp Val Ala Asp Leu Glu Arg Gly Phe Leu Glu Lys Pro Lys  
115 120 125  
Gln Val Glu Met Gly Lys Lys Leu Glu Lys Lys Val Lys Tyr Phe Asn  
130 135 140  
Glu Glu Ala Glu Arg His Leu Glu Thr Leu Asp Gly Met Asn Ile Ile  
145 150 155 160

Thr Glu Thr Thr Pro Glu Asn Gln Ala Lys Arg Asn Arg Glu Lys Arg  
165 170 175

Lys Thr Leu Val Asn Gly Ile Gln Thr Leu Leu Asn Gln Asn Asp Ala  
180 185 190

Leu Leu Arg Arg Leu Gln Glu Tyr Gln Ser Val Leu Asn Gly Asp Ile  
195 200 205

Pro Glu  
210

<210> 13  
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<213> Caenorhabditis elegans

<220>  
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<222> (1)..(1377)

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1 5 10 15  
cat agt cga agt aac tcc tcg tct tct gtt gac aac gat cga aat caa 96  
His Ser Arg Ser Asn Ser Ser Ser Ser Val Asp Asn Asp Arg Asn Gln  
20 25 30  
cca cca cag cag cca cct caa ccg caa cca caa cag caa tct cag caa 144  
Pro Pro Gln Gln Pro Pro Gln Pro Gln Pro Gln Gln Gln Ser Gln Gln  
35 40 45  
caa tac cag cag gct cca aac gtg aat acc aat atg cat cat tcc aac 192  
Gln Tyr Gln Gln Ala Pro Asn Val Asn Thr Asn Met His His Ser Asn  
50 55 60  
gga ttc tca cct aac ttc cca tct cgt agt cct att ccg gac ttt ccc 240  
Gly Phe Ser Pro Asn Phe Pro Ser Arg Ser Pro Ile Pro Asp Phe Pro  
65 70 75 80  
agt ttt tca tct ggg ttc cca aac gat tct gaa tgg tct tcg aat ttc 288  
Ser Phe Ser Ser Gly Phe Pro Asn Asp Ser Glu Trp Ser Ser Asn Phe  
85 90 95  
ccg tcg ttt cca aat ttc cca agt gga ttc tca aat gga agt tct aat 336

Pro Ser Phe Pro Asn Phe Pro Ser Gly Phe Ser Asn Gly Ser Ser Asn	
100 105 110	
ttc cct gat ttt cca aga ttc gga aga gat gga gga cta tcg cca aac	384
Phe Pro Asp Phe Pro Arg Phe Gly Arg Asp Gly Gly Leu Ser Pro Asn	
115 120 125	
cca ccg atg caa gga tac agg aga agt cca aca cca aca tca act caa	432
Pro Pro Met Gln Gly Tyr Arg Arg Ser Pro Thr Pro Thr Ser Thr Gln	
130 135 140	
tct cca act tct aca tta aga cgc aac tct cag cag aat caa gct cct	480
Ser Pro Thr Ser Thr Leu Arg Arg Asn Ser Gln Gln Asn Gln Ala Pro	
145 150 155 160	
cca caa tat tct cag caa caa cca caa caa gct caa caa cgt cag aca	528
Pro Gln Tyr Ser Gln Gln Gln Pro Gln Gln Ala Gln Gln Arg Gln Thr	
165 170 175	
act cct ccg tca aca aaa gct tca tct cga cca cca tct cgt act cgt	576
Thr Pro Pro Ser Thr Lys Ala Ser Ser Arg Pro Pro Ser Arg Thr Arg	
180 185 190	
gaa cca aag gaa cct gag gta ccc gag aga cca gca gtt att cca ttg	624
Glu Pro Lys Glu Pro Glu Val Pro Glu Arg Pro Ala Val Ile Pro Leu	
195 200 205	
cca tat gag aag aag gag aaa cca ctg gag aag aaa ggt agt cgt gat	672
Pro Tyr Glu Lys Lys Glu Lys Pro Leu Glu Lys Lys Gly Ser Arg Asp	
210 215 220	
tct gga aag ggt gat gag aac ctt gaa gag aac att gcc aag atc acg	720
Ser Gly Lys Gly Asp Glu Asn Leu Glu Glu Asn Ile Ala Lys Ile Thr	
225 230 235 240	
atc gga aag aat aat tgc gag tta tgt ccg gaa caa gaa acg gac ggc	768
Ile Gly Lys Asn Asn Cys Glu Leu Cys Pro Glu Gln Glu Thr Asp Gly	
245 250 255	
gac cca tct cca cta acc tcc cca atc acc gaa gga aag cca aag aga	816
Asp Pro Ser Pro Leu Thr Ser Pro Ile Thr Glu Gly Lys Pro Lys Arg	
260 265 270	
gga aag aaa ctt caa cgt aat caa agt gtt gtt gat ttc aat gcc aag	864
Gly Lys Lys Leu Gln Arg Asn Gln Ser Val Val Asp Phe Asn Ala Lys	
275 280 285	
aca att gtt act ttg gat aaa att gaa tta caa gtt gag cag ttg aga	912

Thr	Ile	Val	Thr	Leu	Asp	Lys	Ile	Glu	Leu	Gln	Val	Glu	Gln	Leu	Arg		
290						295					300						
aaa	aaa	gct	gct	gaa	ctc	gaa	atg	gaa	aaa	gag	caa	att	ctt	cgt	tct	960	
Lys	Lys	Ala	Ala	Glu	Leu	Glu	Met	Glu	Lys	Glu	Gln	Ile	Leu	Arg	Ser		
305				310						315					320		
cta	gga	gaa	atc	agt	gtt	cat	aac	tgc	atg	ttc	aaa	ctg	gaa	gaa	tgt	1008	
Leu	Gly	Glu	Ile	Ser	Val	His	Asn	Cys	Met	Phe	Lys	Leu	Glu	Glu	Cys		
				325					330					335			
gat	cgt	gaa	gag	att	gaa	gca	atc	act	gac	cga	ttg	aca	aaa	aga	aca	1056	
Asp	Arg	Glu	Glu	Ile	Glu	Ala	Ile	Thr	Asp	Arg	Leu	Thr	Lys	Arg	Thr		
				340				345					350				
aag	aca	gtt	caa	gtt	gtt	gtc	gaa	act	cca	cga	aat	gaa	gaa	cag	aaa	1104	
Lys	Thr	Val	Gln	Val	Val	Val	Glu	Thr	Pro	Arg	Asn	Glu	Glu	Gln	Lys		
		355					360					365					
aaa	gca	ctg	gaa	gat	gca	act	ttg	atg	atc	gat	gaa	gtc	gga	gaa	atg	1152	
Lys	Ala	Leu	Glu	Asp	Ala	Thr	Leu	Met	Ile	Asp	Glu	Val	Gly	Glu	Met		
	370					375				380							
atg	cat	tcg	aat	att	gaa	aag	gct	aag	ctg	tgc	cta	caa	acc	tac	atg	1200	
Met	His	Ser	Asn	Ile	Glu	Lys	Ala	Lys	Leu	Cys	Leu	Gln	Thr	Tyr	Met		
385				390						395					400		
aac	gcc	tgt	tcg	tac	gaa	gaa	act	gct	gga	gcc	acc	tgc	caa	aac	ttc	1248	
Asn	Ala	Cys	Ser	Tyr	Glu	Glu	Thr	Ala	Gly	Ala	Thr	Cys	Gln	Asn	Phe		
				405					410				415				
ttg	aag	atc	ata	att	cag	tgc	gct	gct	gat	gat	cag	aaa	cgc	atc	aag	1296	
Leu	Lys	Ile	Ile	Ile	Gln	Cys	Ala	Ala	Asp	Asp	Gln	Lys	Arg	Ile	Lys		
			420				425					430					
cgt	cgt	ctg	gaa	aat	ctg	atg	tct	caa	att	gag	aat	gct	gag	aga	acg	1344	
Arg	Arg	Leu	Glu	Asn	Leu	Met	Ser	Gln	Ile	Glu	Asn	Ala	Glu	Arg	Thr		
		435				440					445						
aaa	gca	gat	ttg	atg	gat	gat	caa	agc	gaa	tag						1377	
Lys	Ala	Asp	Leu	Met	Asp	Asp	Gln	Ser	Glu								
	450				455												

<210> 14

<211> 458

<212> PRT

<213> Caenorhabditis elegans

<400> 14

Met Pro Val Val Asn Ile Pro Ile Lys Ile Leu Gly Gln Asn Gln Ser  
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His Ser Arg Ser Asn Ser Ser Ser Ser Val Asp Asn Asp Arg Asn Gln  
20 25 30

Pro Pro Gln Gln Pro Pro Gln Pro Gln Pro Gln Gln Gln Ser Gln Gln  
35 40 45

Gln Tyr Gln Gln Ala Pro Asn Val Asn Thr Asn Met His His Ser Asn  
50 55 60

Gly Phe Ser Pro Asn Phe Pro Ser Arg Ser Pro Ile Pro Asp Phe Pro  
65 70 75 80

Ser Phe Ser Ser Gly Phe Pro Asn Asp Ser Glu Trp Ser Ser Asn Phe  
85 90 95

Pro Ser Phe Pro Asn Phe Pro Ser Gly Phe Ser Asn Gly Ser Ser Asn  
100 105 110

Phe Pro Asp Phe Pro Arg Phe Gly Arg Asp Gly Gly Leu Ser Pro Asn  
115 120 125

Pro Pro Met Gln Gly Tyr Arg Arg Ser Pro Thr Pro Thr Ser Thr Gln  
130 135 140

Ser Pro Thr Ser Thr Leu Arg Arg Asn Ser Gln Gln Asn Gln Ala Pro  
145 150 155 160

Pro Gln Tyr Ser Gln Gln Gln Pro Gln Gln Ala Gln Gln Arg Gln Thr  
165 170 175

Thr Pro Pro Ser Thr Lys Ala Ser Ser Arg Pro Pro Ser Arg Thr Arg  
180 185 190

Glu Pro Lys Glu Pro Glu Val Pro Glu Arg Pro Ala Val Ile Pro Leu  
195 200 205

Pro Tyr Glu Lys Lys Glu Lys Pro Leu Glu Lys Lys Gly Ser Arg Asp  
210 215 220

Ser Gly Lys Gly Asp Glu Asn Leu Glu Glu Asn Ile Ala Lys Ile Thr  
225 230 235 240

Ile Gly Lys Asn Asn Cys Glu Leu Cys Pro Glu Gln Glu Thr Asp Gly



	245		250		255
Asp Pro Ser Pro Leu Thr Ser Pro Ile Thr Glu Gly Lys Pro Lys Arg					
	260		265		270
Gly Lys Lys Leu Gln Arg Asn Gln Ser Val Val Asp Phe Asn Ala Lys					
	275		280		285
Thr Ile Val Thr Leu Asp Lys Ile Glu Leu Gln Val Glu Gln Leu Arg					
	290		295		300
Lys Lys Ala Ala Glu Leu Glu Met Glu Lys Glu Gln Ile Leu Arg Ser					
305		310		315	320
Leu Gly Glu Ile Ser Val His Asn Cys Met Phe Lys Leu Glu Glu Cys					
	325		330		335
Asp Arg Glu Glu Ile Glu Ala Ile Thr Asp Arg Leu Thr Lys Arg Thr					
	340		345		350
Lys Thr Val Gln Val Val Val Glu Thr Pro Arg Asn Glu Glu Gln Lys					
	355		360		365
Lys Ala Leu Glu Asp Ala Thr Leu Met Ile Asp Glu Val Gly Glu Met					
	370		375		380
Met His Ser Asn Ile Glu Lys Ala Lys Leu Cys Leu Gln Thr Tyr Met					
385		390		395	400
Asn Ala Cys Ser Tyr Glu Glu Thr Ala Gly Ala Thr Cys Gln Asn Phe					
	405		410		415
Leu Lys Ile Ile Ile Gln Cys Ala Ala Asp Asp Gln Lys Arg Ile Lys					
	420		425		430
Arg Arg Leu Glu Asn Leu Met Ser Gln Ile Glu Asn Ala Glu Arg Thr					
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Lys Ala Asp Leu Met Asp Asp Gln Ser Glu					
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<212> DNA

<213> Schizosaccharomyces pombe

<220>

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<222> (1)..(588)

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Met Ser Glu Lys Thr Ser Thr Val Thr Ile His Tyr Gly Asn Gln Arg

1

5

10

15

ttt ccg gta gca gtc aat cta aat gag acg tta agt gaa ctg att gat 96

Phe Pro Val Ala Val Asn Leu Asn Glu Thr Leu Ser Glu Leu Ile Asp

20

25

30

gat tta ctt gaa acg act gag att tct gag aag aaa gtc aag ctt ttt 144

Asp Leu Leu Glu Thr Thr Glu Ile Ser Glu Lys Lys Val Lys Leu Phe

35

40

45

tac gct ggc aag cgt tta aaa gac aaa aaa gcc tcg tta tca aaa ttg 192

Tyr Ala Gly Lys Arg Leu Lys Asp Lys Lys Ala Ser Leu Ser Lys Leu

50

55

60

ggt tta aaa aat cat agt aaa att cta tgt ata aga cca cat aag caa 240

Gly Leu Lys Asn His Ser Lys Ile Leu Cys Ile Arg Pro His Lys Gln

65

70

75

80

caa cga ggt tcc aag gaa aaa gac acg gtt gag ccc gct ccg aaa gcg 288

Gln Arg Gly Ser Lys Glu Lys Asp Thr Val Glu Pro Ala Pro Lys Ala

85

90

95

gaa gcg gag aat cct gta ttt tcg cgt att tct gga gaa ata aaa gcc 336

Glu Ala Glu Asn Pro Val Phe Ser Arg Ile Ser Gly Glu Ile Lys Ala

100

105

110

atc gat cag tat gtt gac aaa gaa ctt tcc ccc atg tac gac aat tac 384

Ile Asp Gln Tyr Val Asp Lys Glu Leu Ser Pro Met Tyr Asp Asn Tyr

115

120

125

gta aat aaa ccg tcg aac gat cca aag cag aaa aac aaa cag aaa cta 432

Val Asn Lys Pro Ser Asn Asp Pro Lys Gln Lys Asn Lys Gln Lys Leu

130

135

140

atg ata agt gaa cta ctt tta caa cag ctt tta aaa ttg gat gga gtt 480

Met Ile Ser Glu Leu Leu Leu Gln Gln Leu Leu Lys Leu Asp Gly Val

145

150

155

160

gac gta ctg ggc agc gag aaa ttg cgt ttt gaa cgg aag caa ctt gtt 528

Asp Val Leu Gly Ser Glu Lys Leu Arg Phe Glu Arg Lys Gln Leu Val

165

170

175

tct aag atc caa aaa atg ttg gat cac gtt gac caa aca agc caa gaa 576  
 Ser Lys Ile Gln Lys Met Leu Asp His Val Asp Gln Thr Ser Gln Glu  
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gtg gcc gca tag 588  
 Val Ala Ala  
           195

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 <213> Schizosaccharomyces pombe

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Phe Pro Val Ala Val Asn Leu Asn Glu Thr Leu Ser Glu Leu Ile Asp  
                   20                          25                          30

Asp Leu Leu Glu Thr Thr Glu Ile Ser Glu Lys Lys Val Lys Leu Phe  
           35                          40                          45

Tyr Ala Gly Lys Arg Leu Lys Asp Lys Lys Ala Ser Leu Ser Lys Leu  
       50                          55                          60

Gly Leu Lys Asn His Ser Lys Ile Leu Cys Ile Arg Pro His Lys Gln  
       65                          70                          75                          80

Gln Arg Gly Ser Lys Glu Lys Asp Thr Val Glu Pro Ala Pro Lys Ala  
                   85                          90                          95

Glu Ala Glu Asn Pro Val Phe Ser Arg Ile Ser Gly Glu Ile Lys Ala  
                   100                          105                          110

Ile Asp Gln Tyr Val Asp Lys Glu Leu Ser Pro Met Tyr Asp Asn Tyr  
           115                          120                          125

Val Asn Lys Pro Ser Asn Asp Pro Lys Gln Lys Asn Lys Gln Lys Leu  
       130                          135                          140

Met Ile Ser Glu Leu Leu Leu Gln Gln Leu Leu Lys Leu Asp Gly Val  
       145                          150                          155                          160

Asp Val Leu Gly Ser Glu Lys Leu Arg Phe Glu Arg Lys Gln Leu Val  
                   165                          170                          175

Ser Lys Ile Gln Lys Met Leu Asp His Val Asp Gln Thr Ser Gln Glu  
180 185 190

Val Ala Ala  
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1 5 10 15  
tct cta gct gta ttg tca gtt act gtt ttg att agc gca tta ttg aaa 96  
Ser Leu Ala Val Leu Ser Val Thr Val Leu Ile Ser Ala Leu Leu Lys  
20 25 30  
aag aga gct act gaa acc gaa gat att gtc gtt gtt cat tac gat ggc 144  
Lys Arg Ala Thr Glu Thr Glu Asp Ile Val Val Val His Tyr Asp Gly  
35 40 45  
gaa aag ttg aat ttt gtg ttg cga caa cca agg ctg aat atg gtt tct 192  
Glu Lys Leu Asn Phe Val Leu Arg Gln Pro Arg Leu Asn Met Val Ser  
50 55 60  
tac act agt ttt ctt cgt cgc gtg tgc aac gca ttt tca gta atg ccc 240  
Tyr Thr Ser Phe Leu Arg Arg Val Cys Asn Ala Phe Ser Val Met Pro  
65 70 75 80  
gac aaa gcg tct ctc aag tta aac ggg gtg acc ctc aag gat ggt tca 288  
Asp Lys Ala Ser Leu Lys Leu Asn Gly Val Thr Leu Lys Asp Gly Ser  
85 90 95  
ctt tcc gac caa aat gtg caa aat gga agt gaa tta gag ctc gaa tta 336  
Leu Ser Asp Gln Asn Val Gln Asn Gly Ser Glu Leu Glu Leu Glu Leu  
100 105 110  
ccc aaa ctg agc ccg gca atg caa caa att gaa gca tat ata gat gag 384  
Pro Lys Leu Ser Pro Ala Met Gln Gln Ile Glu Ala Tyr Ile Asp Glu  
115 120 125

ctt caa cag gat ctg gtc cct aaa att gaa gcc ttc tgc caa tcg tct 432  
 Leu Gln Gln Asp Leu Val Pro Lys Ile Glu Ala Phe Cys Gln Ser Ser  
 130 135 140

ccc gct tcg gca caa gat gtt caa gat ttg cat aca cgc ctt agt gaa 480  
 Pro Ala Ser Ala Gln Asp Val Gln Asp Leu His Thr Arg Leu Ser Glu  
 145 150 155 160

aca ttg ttg gct agg atg ata aaa tta gat gct gtt aat gtt gaa gac 528  
 Thr Leu Leu Ala Arg Met Ile Lys Leu Asp Ala Val Asn Val Glu Asp  
 165 170 175

gac cca gaa gct cgt ctt aaa aga aaa gaa gct att cgt tta tct caa 576  
 Asp Pro Glu Ala Arg Leu Lys Arg Lys Glu Ala Ile Arg Leu Ser Gln  
 180 185 190

caa tat ttg agt aaa cta gat tcc acc aag aat caa aac aaa tga 621  
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 195 200 205

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<212> PRT

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 20 25 30

Lys Arg Ala Thr Glu Thr Glu Asp Ile Val Val Val His Tyr Asp Gly  
 35 40 45

Glu Lys Leu Asn Phe Val Leu Arg Gln Pro Arg Leu Asn Met Val Ser  
 50 55 60

Tyr Thr Ser Phe Leu Arg Arg Val Cys Asn Ala Phe Ser Val Met Pro  
 65 70 75 80

Asp Lys Ala Ser Leu Lys Leu Asn Gly Val Thr Leu Lys Asp Gly Ser  
 85 90 95

Leu Ser Asp Gln Asn Val Gln Asn Gly Ser Glu Leu Glu Leu Glu Leu  
 100 105 110

Pro Lys Leu Ser Pro Ala Met Gln Gln Ile Glu Ala Tyr Ile Asp Glu  
 115 120 125

Leu Gln Gln Asp Leu Val Pro Lys Ile Glu Ala Phe Cys Gln Ser Ser  
 130 135 140

Pro Ala Ser Ala Gln Asp Val Gln Asp Leu His Thr Arg Leu Ser Glu  
 145 150 155 160

Thr Leu Leu Ala Arg Met Ile Lys Leu Asp Ala Val Asn Val Glu Asp  
 165 170 175

Asp Pro Glu Ala Arg Leu Lys Arg Lys Glu Ala Ile Arg Leu Ser Gln  
 180 185 190

Gln Tyr Leu Ser Lys Leu Asp Ser Thr Lys Asn Gln Asn Lys  
 195 200 205

<210> 19

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<212> DNA

<213> Homo sapiens

<220>

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atttccagac acttccaccc ctctctggcc acgtcacccc cgcctttaat tcataaaggt 180

gcccggcgcc ggcttcccgg acacgtcggc ggccgagagg ggcccacggc ggccggcccgg 240

ccagagactc ggccggcgga gccagcgccc cgcacccgcg cccagcggg cagaccgcaa 300

cccagc atg agc gcc gcc acc cac tcg ccc atg atg cag gtg gcg tcc 348

Met Ser Ala Ala Thr His Ser Pro Met Met Gln Val Ala Ser  
 1 5 10

ggc aac ggt gac cgc gac cct ttg ccc ccc gga tgg gag atc aag atc 396

Gly Asn Gly Asp Arg Asp Pro Leu Pro Pro Gly Trp Glu Ile Lys Ile  
 15 20 25 30

gac ccg cag acc ggc tgg ccc ttc ttc gtg gac cac aac agc cgc acc	444
Asp Pro Gln Thr Gly Trp Pro Phe Phe Val Asp His Asn Ser Arg Thr	
35 40 45	
act acg tgg aac gac ccg cgc gtg ccc tct gag ggc ccc aag gag act	492
Thr Thr Trp Asn Asp Pro Arg Val Pro Ser Glu Gly Pro Lys Glu Thr	
50 55 60	
cca tcc tct gcc aat ggc cct tcc cgg gag ggc tct agg ctg ccg cct	540
Pro Ser Ser Ala Asn Gly Pro Ser Arg Glu Gly Ser Arg Leu Pro Pro	
65 70 75	
gct agg gaa ggc cac cct gtg tac ccc cag ctc cga cca ggc tac att	588
Ala Arg Glu Gly His Pro Val Tyr Pro Gln Leu Arg Pro Gly Tyr Ile	
80 85 90	
ccc att cct gtg ctc cat gaa ggc gct gag aac cgg cag gtg cac cct	636
Pro Ile Pro Val Leu His Glu Gly Ala Glu Asn Arg Gln Val His Pro	
95 100 105 110	
ttc cat gtc tat ccc cag cct ggg atg cag cga ttc cga act gag gcg	684
Phe His Val Tyr Pro Gln Pro Gly Met Gln Arg Phe Arg Thr Glu Ala	
115 120 125	
gca gca gcg gct cct cag agg tcc cag tca cct ctg cgg ggc atg cca	732
Ala Ala Ala Ala Pro Gln Arg Ser Gln Ser Pro Leu Arg Gly Met Pro	
130 135 140	
gaa acc act cag cca gat aaa cag tgt gga cag gtg gca gcg gcg gcg	780
Glu Thr Thr Gln Pro Asp Lys Gln Cys Gly Gln Val Ala Ala Ala Ala	
145 150 155	
gca gcc cag ccc cca gcc tcc cac gga cct gag cgg tcc cag tct cca	828
Ala Ala Gln Pro Pro Ala Ser His Gly Pro Glu Arg Ser Gln Ser Pro	
160 165 170	
gct gcc tct gac tgc tca tcc tca tcc tcc tcg gcc agc ctg cct tcc	876
Ala Ala Ser Asp Cys Ser Ser Ser Ser Ser Ser Ala Ser Leu Pro Ser	
175 180 185 190	
tcc ggc agg agc agc ctg ggc agt cac cag ctc ccg cgg ggg tac atc	924
Ser Gly Arg Ser Ser Leu Gly Ser His Gln Leu Pro Arg Gly Tyr Ile	
195 200 205	
tcc att ccg gtg ata cac gag cag aac gtt acc cgg cca gca gcc cag	972
Ser Ile Pro Val Ile His Glu Gln Asn Val Thr Arg Pro Ala Ala Gln	
210 215 220	

ccc tcc ttc cac aaa gcc cag aag acg cac tac cca gcg cag agg ggt	1020
Pro Ser Phe His Lys Ala Gln Lys Thr His Tyr Pro Ala Gln Arg Gly	
225 230 235	
gag tac cag acc cac cag cct gtg tac cac aag atc cag ggg gat gac	1068
Glu Tyr Gln Thr His Gln Pro Val Tyr His Lys Ile Gln Gly Asp Asp	
240 245 250	
tgg gag ccc cgg ccc ctg cgg gcg gca tcc ccg ttc agg tca tct gtc	1116
Trp Glu Pro Arg Pro Leu Arg Ala Ala Ser Pro Phe Arg Ser Ser Val	
255 260 265 270	
cag ggt gca tcg agc cgg gag ggc tca cca gcc agg agc agc acg cca	1164
Gln Gly Ala Ser Ser Arg Glu Gly Ser Pro Ala Arg Ser Ser Thr Pro	
275 280 285	
ctc cac tcc ccc tcg ccc atc cgt gtg cac acc gtg gtc gac agg cct	1212
Leu His Ser Pro Ser Pro Ile Arg Val His Thr Val Val Asp Arg Pro	
290 295 300	
cag cag ccc atg acc cat cga gaa act gca cct gtt tcc cag cct gaa	1260
Gln Gln Pro Met Thr His Arg Glu Thr Ala Pro Val Ser Gln Pro Glu	
305 310 315	
aac aaa cca gaa agt aag cca ggc cca gtt gga cca gaa ctc cct cct	1308
Asn Lys Pro Glu Ser Lys Pro Gly Pro Val Gly Pro Glu Leu Pro Pro	
320 325 330	
gga cac atc cca att caa gtg atc cgc aaa gag gtg gat tct aaa cct	1356
Gly His Ile Pro Ile Gln Val Ile Arg Lys Glu Val Asp Ser Lys Pro	
335 340 345 350	
gtt tcc cag aag ccc cca cct ccc tct gag aag gta gag gtg aaa gtt	1404
Val Ser Gln Lys Pro Pro Pro Pro Ser Glu Lys Val Glu Val Lys Val	
355 360 365	
ccc cct gct cca gtt cct tgt cct cct ccc agc cct ggc cct tct gct	1452
Pro Pro Ala Pro Val Pro Cys Pro Pro Pro Ser Pro Gly Pro Ser Ala	
370 375 380	
gtc ccc tct tcc ccc aag agt gtg gct aca gaa gag agg gca gcc ccc	1500
Val Pro Ser Ser Pro Lys Ser Val Ala Thr Glu Glu Arg Ala Ala Pro	
385 390 395	
agc act gcc cct gca gaa gct aca cct cca aaa cca gga gaa gcc gag	1548
Ser Thr Ala Pro Ala Glu Ala Thr Pro Pro Lys Pro Gly Glu Ala Glu	
400 405 410	



gct ccc cca aaa cat cca gga gtg ctg aaa gtg gaa gcc atc ctg gag 1596  
Ala Pro Pro Lys His Pro Gly Val Leu Lys Val Glu Ala Ile Leu Glu  
415 420 425 430

aag gtg cag ggg ctg gag cag gct gta gac aac ttt gaa ggc aag aag 1644  
Lys Val Gln Gly Leu Glu Gln Ala Val Asp Asn Phe Glu Gly Lys Lys  
435 440 445

act gac aaa aag tac ctg atg atc gaa gag tat ttg acc aaa gag ctg 1692  
Thr Asp Lys Lys Tyr Leu Met Ile Glu Glu Tyr Leu Thr Lys Glu Leu  
450 455 460

ctg gcc ctg gat tca gtg gac ccc gag gga cga gcc gat gtg cgt cag 1740  
Leu Ala Leu Asp Ser Val Asp Pro Glu Gly Arg Ala Asp Val Arg Gln  
465 470 475

gcc agg aga gac ggt gtc agg aag gtt cag acc atc ttg gaa aaa ctt 1788  
Ala Arg Arg Asp Gly Val Arg Lys Val Gln Thr Ile Leu Glu Lys Leu  
480 485 490

gaa cag aaa gcc att gat gtc cca ggt caa gtc cag gtc tat gaa ctc 1836  
Glu Gln Lys Ala Ile Asp Val Pro Gly Gln Val Gln Val Tyr Glu Leu  
495 500 505 510

cag ccc agc aac ctt gaa gca gat cag cca ctg cag gca atc atg gag 1884  
Gln Pro Ser Asn Leu Glu Ala Asp Gln Pro Leu Gln Ala Ile Met Glu  
515 520 525

atg ggt gcc gtg gca gca gac aag ggc aag aaa aat gct gga aat gca 1932  
Met Gly Ala Val Ala Ala Asp Lys Gly Lys Lys Asn Ala Gly Asn Ala  
530 535 540

gaa gat ccc cac aca gaa acc cag cag cca gaa gcc aca gca gca gcg 1980  
Glu Asp Pro His Thr Glu Thr Gln Gln Pro Glu Ala Thr Ala Ala Ala  
545 550 555

act tca aac ccc agc agc atg aca gac acc cct ggt aac cca gca gca 2028  
Thr Ser Asn Pro Ser Ser Met Thr Asp Thr Pro Gly Asn Pro Ala Ala  
560 565 570

ccg tag cctctgccct gtaaaaatca gactcggaac cgatgtgtgc tttagggaat 2084  
Pro  
575

tttaagttgc atgcatttca gagacttta gtcagttggt ttttattagc tgcttggtat 2144

gcagtaactt gggtggaggc aaaacactaa taaaagggct aaaaaggaaa atgatgcttt 2204

tcttctatat tcttactctg tacaaataaa gaagttgctt gttgtttgag aagtttaacc 2264  
 ccgttgcttg ttctgcagcc ctgtctactt gggcaccccc accacctgtt agctgtggtt 2324  
 gtgcactgtc tttttagct ctggactgga ggggtagatg gggagtcaat tacccatcac 2384  
 ataaatatga aacatttatc agaaatgttg ccattttaat gagatgattt tcttcatctc 2444  
 ataattaaata tacctgactt tagagagagt aaaatgtgcc aggagccata ggaatatctg 2504  
 tatgttggat gactttaatg ctacattttc 2534

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 <212> PRT  
 <213> Homo sapiens

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 Gln Thr Gly Trp Pro Phe Phe Val Asp His Asn Ser Arg Thr Thr Thr  
 35 40 45  
 Trp Asn Asp Pro Arg Val Pro Ser Glu Gly Pro Lys Glu Thr Pro Ser  
 50 55 60  
 Ser Ala Asn Gly Pro Ser Arg Glu Gly Ser Arg Leu Pro Pro Ala Arg  
 65 70 75 80  
 Glu Gly His Pro Val Tyr Pro Gln Leu Arg Pro Gly Tyr Ile Pro Ile  
 85 90 95  
 Pro Val Leu His Glu Gly Ala Glu Asn Arg Gln Val His Pro Phe His  
 100 105 110  
 Val Tyr Pro Gln Pro Gly Met Gln Arg Phe Arg Thr Glu Ala Ala Ala  
 115 120 125  
 Ala Ala Pro Gln Arg Ser Gln Ser Pro Leu Arg Gly Met Pro Glu Thr  
 130 135 140  
 Thr Gln Pro Asp Lys Gln Cys Gly Gln Val Ala Ala Ala Ala Ala Ala  
 145 150 155 160

Gln Pro Pro Ala Ser His Gly Pro Glu Arg Ser Gln Ser Pro Ala Ala  
 165 170 175

Ser Asp Cys Ser Ser Ser Ser Ser Ser Ala Ser Leu Pro Ser Ser Gly  
 180 185 190

Arg Ser Ser Leu Gly Ser His Gln Leu Pro Arg Gly Tyr Ile Ser Ile  
 195 200 205

Pro Val Ile His Glu Gln Asn Val Thr Arg Pro Ala Ala Gln Pro Ser  
 210 215 220

Phe His Lys Ala Gln Lys Thr His Tyr Pro Ala Gln Arg Gly Glu Tyr  
 225 230 235 240

Gln Thr His Gln Pro Val Tyr His Lys Ile Gln Gly Asp Asp Trp Glu  
 245 250 255

Pro Arg Pro Leu Arg Ala Ala Ser Pro Phe Arg Ser Ser Val Gln Gly  
 260 265 270

Ala Ser Ser Arg Glu Gly Ser Pro Ala Arg Ser Ser Thr Pro Leu His  
 275 280 285

Ser Pro Ser Pro Ile Arg Val His Thr Val Val Asp Arg Pro Gln Gln  
 290 295 300

Pro Met Thr His Arg Glu Thr Ala Pro Val Ser Gln Pro Glu Asn Lys  
 305 310 315 320

Pro Glu Ser Lys Pro Gly Pro Val Gly Pro Glu Leu Pro Pro Gly His  
 325 330 335

Ile Pro Ile Gln Val Ile Arg Lys Glu Val Asp Ser Lys Pro Val Ser  
 340 345 350

Gln Lys Pro Pro Pro Pro Ser Glu Lys Val Glu Val Lys Val Pro Pro  
 355 360 365

Ala Pro Val Pro Cys Pro Pro Pro Ser Pro Gly Pro Ser Ala Val Pro  
 370 375 380

Ser Ser Pro Lys Ser Val Ala Thr Glu Glu Arg Ala Ala Pro Ser Thr  
 385 390 395 400

Ala Pro Ala Glu Ala Thr Pro Pro Lys Pro Gly Glu Ala Glu Ala Pro  
 405 410 415

Pro Lys His Pro Gly Val Leu Lys Val Glu Ala Ile Leu Glu Lys Val  
 420 425 430

Gln Gly Leu Glu Gln Ala Val Asp Asn Phe Glu Gly Lys Lys Thr Asp  
 435 440 445

Lys Lys Tyr Leu Met Ile Glu Glu Tyr Leu Thr Lys Glu Leu Leu Ala  
 450 455 460

Leu Asp Ser Val Asp Pro Glu Gly Arg Ala Asp Val Arg Gln Ala Arg  
 465 470 475 480

Arg Asp Gly Val Arg Lys Val Gln Thr Ile Leu Glu Lys Leu Glu Gln  
 485 490 495

Lys Ala Ile Asp Val Pro Gly Gln Val Gln Val Tyr Glu Leu Gln Pro  
 500 505 510

Ser Asn Leu Glu Ala Asp Gln Pro Leu Gln Ala Ile Met Glu Met Gly  
 515 520 525

Ala Val Ala Ala Asp Lys Gly Lys Lys Asn Ala Gly Asn Ala Glu Asp  
 530 535 540

Pro His Thr Glu Thr Gln Gln Pro Glu Ala Thr Ala Ala Ala Thr Ser  
 545 550 555 560

Asn Pro Ser Ser Met Thr Asp Thr Pro Gly Asn Pro Ala Ala Pro  
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<211> 1966

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (43)..(1416)

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 Arg Arg Ser Gly Tyr Gly Pro Ser Asp Gly Pro Ser Tyr Gly Arg Tyr

5	10	15	20	
tac ggg cct ggg ggt gga gat gtg ccg gta cac cca cct cca ccc tta				150
Tyr Gly Pro Gly Gly Gly Asp Val Pro Val His Pro Pro Pro Pro Leu				
	25	30	35	
tat cct ctt cgc cct gaa cct ccc cag cct ccc att tcc tgg cgg gtg				198
Tyr Pro Leu Arg Pro Glu Pro Pro Gln Pro Pro Ile Ser Trp Arg Val				
	40	45	50	
cgc ggg ggc ggc ccg gcg gag acc acc tgg ctg gga gaa ggc gga gga				246
Arg Gly Gly Gly Pro Ala Glu Thr Thr Trp Leu Gly Glu Gly Gly Gly				
	55	60	65	
ggc gat ggc tac tat ccc tcg gga ggc gcc tgg cca gag cct ggt cga				294
Gly Asp Gly Tyr Tyr Pro Ser Gly Gly Ala Trp Pro Glu Pro Gly Arg				
	70	75	80	
gcc gga gga agc cac cag gag cag cca cca tat cct agc tac aat tct				342
Ala Gly Gly Ser His Gln Glu Gln Pro Pro Tyr Pro Ser Tyr Asn Ser				
	85	90	95	100
aac tat tgg aat tct act gcg aga tct agg gct cct tac cca agt aca				390
Asn Tyr Trp Asn Ser Thr Ala Arg Ser Arg Ala Pro Tyr Pro Ser Thr				
	105	110	115	
tat cct gta aga cca gaa ttg caa ggc cag agt ttg aat tct tat aca				438
Tyr Pro Val Arg Pro Glu Leu Gln Gly Gln Ser Leu Asn Ser Tyr Thr				
	120	125	130	
aat gga gcg tat ggt cca aca tac ccc cca ggc cct ggg gca aat act				486
Asn Gly Ala Tyr Gly Pro Thr Tyr Pro Pro Gly Pro Gly Ala Asn Thr				
	135	140	145	
gcc tca tac tca ggg gct tat tat gca cct ggt tat act cag acc agt				534
Ala Ser Tyr Ser Gly Ala Tyr Tyr Ala Pro Gly Tyr Thr Gln Thr Ser				
	150	155	160	
tac tcc aca gaa gtt cca agt act tac cgt tca tct ggc aac agc cca				582
Tyr Ser Thr Glu Val Pro Ser Thr Tyr Arg Ser Ser Gly Asn Ser Pro				
	165	170	175	180
act cca gtc tct cgt tgg atc tat ccc cag cag gac tgt cag act gaa				630
Thr Pro Val Ser Arg Trp Ile Tyr Pro Gln Gln Asp Cys Gln Thr Glu				
	185	190	195	
gca ccc cct ctt agg ggg cag gtt cca gga tat ccg cct tca cag aac				678
Ala Pro Pro Leu Arg Gly Gln Val Pro Gly Tyr Pro Pro Ser Gln Asn				

200	205	210	
cct gga atg acc ctg ccc cat tat cct tat gga gat ggt aat cgt agt			726
Pro Gly Met Thr Leu Pro His Tyr Pro Tyr Gly Asp Gly Asn Arg Ser			
215	220	225	
gtt cca caa tca gga ccg act gta cga cca caa gaa gat gcg tgg gct			774
Val Pro Gln Ser Gly Pro Thr Val Arg Pro Gln Glu Asp Ala Trp Ala			
230	235	240	
tct cct ggt gct tat gga atg ggt ggc cgt tat ccc tgg cct tca tca			822
Ser Pro Gly Ala Tyr Gly Met Gly Gly Arg Tyr Pro Trp Pro Ser Ser			
245	250	255	260
gcg ccc tca gca cca ccc ggc aat ctc tac atg act gaa agt act tca			870
Ala Pro Ser Ala Pro Pro Gly Asn Leu Tyr Met Thr Glu Ser Thr Ser			
265	270	275	
cca tgg cct agc agt ggc tct ccc cag tca ccc cct tca ccc cca gtc			918
Pro Trp Pro Ser Ser Gly Ser Pro Gln Ser Pro Pro Ser Pro Pro Val			
280	285	290	
cag cag ccc aag gat tct tca tac ccc tat agc caa tca gat caa agc			966
Gln Gln Pro Lys Asp Ser Ser Tyr Pro Tyr Ser Gln Ser Asp Gln Ser			
295	300	305	
atg aac cgg cac aac ttt cct tgc agt gtc cat cag tac gaa tcc tcg			1014
Met Asn Arg His Asn Phe Pro Cys Ser Val His Gln Tyr Glu Ser Ser			
310	315	320	
ggg aca gtg atc aat gaa gat tca gat ctt ttg gat tcc caa gtc cag			1062
Gly Thr Val Ile Asn Glu Asp Ser Asp Leu Leu Asp Ser Gln Val Gln			
325	330	335	340
tat agt gct gag cct cag ctg tat ggt aat gcc acc agt gac cat ccc			1110
Tyr Ser Ala Glu Pro Gln Leu Tyr Gly Asn Ala Thr Ser Asp His Pro			
345	350	355	
aac aat caa gat caa agt agc agt ctt cct gaa gaa tgt gta cct tca			1158
Asn Asn Gln Asp Gln Ser Ser Ser Leu Pro Glu Glu Cys Val Pro Ser			
360	365	370	
gat gaa agt act cct ccg agt att aaa aaa atc ata cat gtg ctg gag			1206
Asp Glu Ser Thr Pro Pro Ser Ile Lys Lys Ile Ile His Val Leu Glu			
375	380	385	
aag gtc cag tat ctt gaa caa gaa gta gaa gaa ttt gta gga aaa aag			1254
Lys Val Gln Tyr Leu Glu Gln Glu Val Glu Glu Phe Val Gly Lys Lys			

390	395	400	
aca gac aaa gca tac tgg ctt ctg gaa gaa atg cta acc aag gaa ctt			1302
Thr Asp Lys Ala Tyr Trp Leu Leu Glu Glu Met Leu Thr Lys Glu Leu			
405	410	415	420
ttg gaa ctg gat tca gtt gaa act ggg ggc cag gac tct gta cgg cag			1350
Leu Glu Leu Asp Ser Val Glu Thr Gly Gly Gln Asp Ser Val Arg Gln			
	425	430	435
gcc aga aaa gag gct gtt tgt aag att cag gcc ata ctg gaa aaa tta			1398
Ala Arg Lys Glu Ala Val Cys Lys Ile Gln Ala Ile Leu Glu Lys Leu			
	440	445	450
gaa aaa aaa gga tta tga aaggatttag aacaaagtgg aagcctgtta			1446
Glu Lys Lys Gly Leu			
	455		
ctaacttgac caaagaacac ttgattaggt taattaccct ctttttgaaa tgcctgttga			1506
tgacaagaag caatacattc cagcttttcc tttgatttta tacttgaaaa actggcaaag			1566
gaatggaaga atatttttagt catgaagttg ttttcagttt tcagacgaat gaatgtaata			1626
ggaaactatg gagttaccaa tattgccaag tagactcact ccttaaaaaa tttatggata			1686
tctacaagct gcttattacc agcaggaggg aaacacactt cacacaacag gcttatcaga			1746
aacctaccag atgaaactgg atataatttg agacaaacag gatgtgtttt tttaaacatc			1806
tg gatatctt gtcacatttt tgtacattgt gactgctttc aacatatact tcatgtgtaa			1866
ttatagctta gacttttagcc ttcttggaact tctgttttgt tttgttattt gcagtttaca			1926
aatatagtat tattctctaa aaaaaaaaaa aaaaaaaaaa			1966
<210> 22			
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<212> PRT			
<213> Homo sapiens			
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Met Ser Ala Leu Arg Arg Ser Gly Tyr Gly Pro Ser Asp Gly Pro Ser			
1	5	10	15
Tyr Gly Arg Tyr Tyr Gly Pro Gly Gly Gly Asp Val Pro Val His Pro			
20	25	30	

Pro Pro Pro Leu Tyr Pro Leu Arg Pro Glu Pro Pro Gln Pro Pro Ile  
 35 40 45

Ser Trp Arg Val Arg Gly Gly Gly Pro Ala Glu Thr Thr Trp Leu Gly  
 50 55 60

Glu Gly Gly Gly Gly Asp Gly Tyr Tyr Pro Ser Gly Gly Ala Trp Pro  
 65 70 75 80

Glu Pro Gly Arg Ala Gly Gly Ser His Gln Glu Gln Pro Pro Tyr Pro  
 85 90 95

Ser Tyr Asn Ser Asn Tyr Trp Asn Ser Thr Ala Arg Ser Arg Ala Pro  
 100 105 110

Tyr Pro Ser Thr Tyr Pro Val Arg Pro Glu Leu Gln Gly Gln Ser Leu  
 115 120 125

Asn Ser Tyr Thr Asn Gly Ala Tyr Gly Pro Thr Tyr Pro Pro Gly Pro  
 130 135 140

Gly Ala Asn Thr Ala Ser Tyr Ser Gly Ala Tyr Tyr Ala Pro Gly Tyr  
 145 150 155 160

Thr Gln Thr Ser Tyr Ser Thr Glu Val Pro Ser Thr Tyr Arg Ser Ser  
 165 170 175

Gly Asn Ser Pro Thr Pro Val Ser Arg Trp Ile Tyr Pro Gln Gln Asp  
 180 185 190

Cys Gln Thr Glu Ala Pro Pro Leu Arg Gly Gln Val Pro Gly Tyr Pro  
 195 200 205

Pro Ser Gln Asn Pro Gly Met Thr Leu Pro His Tyr Pro Tyr Gly Asp  
 210 215 220

Gly Asn Arg Ser Val Pro Gln Ser Gly Pro Thr Val Arg Pro Gln Glu  
 225 230 235 240

Asp Ala Trp Ala Ser Pro Gly Ala Tyr Gly Met Gly Gly Arg Tyr Pro  
 245 250 255

Trp Pro Ser Ser Ala Pro Ser Ala Pro Pro Gly Asn Leu Tyr Met Thr  
 260 265 270

Glu Ser Thr Ser Pro Trp Pro Ser Ser Gly Ser Pro Gln Ser Pro Pro  
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Ser Pro Pro Val Gln Gln Pro Lys Asp Ser Ser Tyr Pro Tyr Ser Gln  
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Ser Asp Gln Ser Met Asn Arg His Asn Phe Pro Cys Ser Val His Gln  
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Tyr Glu Ser Ser Gly Thr Val Ile Asn Glu Asp Ser Asp Leu Leu Asp  
 325 330 335

Ser Gln Val Gln Tyr Ser Ala Glu Pro Gln Leu Tyr Gly Asn Ala Thr  
 340 345 350

Ser Asp His Pro Asn Asn Gln Asp Gln Ser Ser Ser Leu Pro Glu Glu  
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Cys Val Pro Ser Asp Glu Ser Thr Pro Pro Ser Ile Lys Lys Ile Ile  
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His Val Leu Glu Lys Val Gln Tyr Leu Glu Gln Glu Val Glu Glu Phe  
 385 390 395 400

Val Gly Lys Lys Thr Asp Lys Ala Tyr Trp Leu Leu Glu Glu Met Leu  
 405 410 415

Thr Lys Glu Leu Leu Glu Leu Asp Ser Val Glu Thr Gly Gly Gln Asp  
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Ser Val Arg Gln Ala Arg Lys Glu Ala Val Cys Lys Ile Gln Ala Ile  
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Leu Glu Lys Leu Glu Lys Lys Gly Leu  
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<212> DNA

<213> Homo sapiens

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aaaagt atg gat atg gga aac caa cat cct tct att agt agg ctt cag 288  
Met Asp Met Gly Asn Gln His Pro Ser Ile Ser Arg Leu Gln  
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Glu Ile Gln Lys Glu Val Lys Ser Val Glu Gln Gln Val Ile Gly Phe  
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Ser Gly Leu Ser Asp Asp Lys Asn Tyr Lys Lys Leu Glu Arg Ile Leu  
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aca aaa cag ctt ttt gaa ata gac tct gta gat act gaa gga aaa gga 432  
Thr Lys Gln Leu Phe Glu Ile Asp Ser Val Asp Thr Glu Gly Lys Gly  
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gat att cag caa gct agg aag cgg gca gca cag gag aca gaa cgt ctt 480  
Asp Ile Gln Gln Ala Arg Lys Arg Ala Ala Gln Glu Thr Glu Arg Leu  
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ctc aaa gag ttg gag cag aat gca aac cac cca cac cgg att gaa ata 528  
Leu Lys Glu Leu Glu Gln Asn Ala Asn His Pro His Arg Ile Glu Ile  
80 85 90  
cag aac att ttt gag gaa gcc cag tcc ctc gtg aga gag aaa att gtg 576  
Gln Asn Ile Phe Glu Glu Ala Gln Ser Leu Val Arg Glu Lys Ile Val  
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Ile Ser Leu Arg Lys Ala Arg Tyr His Thr Leu Thr Lys Ile Cys Ala  
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gtg caa gag ata atc gaa gac tgc atg aaa aag cag cct tcc ctg ccg 768  
Val Gln Glu Ile Ile Glu Asp Cys Met Lys Lys Gln Pro Ser Leu Pro  
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aaa gcc gtc tgg aac gtc ctt gga aac ttg tct gag atc cag gga gaa 1392  
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gaa gag ctg ctc acc aag cag ctg cta gcc ctg gat gct gtt gat ccg 1488  
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 Ala Gln Asn Ile Leu Ser Tyr Leu Asp Leu Lys Ser Asp Glu Trp Glu  
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 Tyr

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Leu Ser Asp Asp Lys Asn Tyr Lys Lys Leu Glu Arg Ile Leu Thr Lys  
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Gln Leu Phe Glu Ile Asp Ser Val Asp Thr Glu Gly Lys Gly Asp Ile  
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Gln Gln Ala Arg Lys Arg Ala Ala Gln Glu Thr Glu Arg Leu Leu Lys  
 65 70 75 80

Glu Leu Glu Gln Asn Ala Asn His Pro His Arg Ile Glu Ile Gln Asn  
 85 90 95

Ile Phe Glu Glu Ala Gln Ser Leu Val Arg Glu Lys Ile Val Pro Phe  
 100 105 110

Tyr Asn Gly Gly Asn Cys Val Thr Asp Glu Phe Glu Glu Gly Ile Gln  
 115 120 125

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Leu	Arg	Lys	Ala	Arg	Tyr	His	Thr	Leu	Thr	Lys	Ile	Cys	Ala	Val	Gln	145	150	155	160
Glu	Ile	Ile	Glu	Asp	Cys	Met	Lys	Lys	Gln	Pro	Ser	Leu	Pro	Leu	Ser	165	170	175	
Glu	Asp	Ala	His	Pro	Ser	Val	Ala	Lys	Ile	Asn	Phe	Val	Met	Cys	Glu	180	185	190	
Val	Asn	Lys	Ala	Arg	Gly	Val	Leu	Ile	Ala	Leu	Leu	Met	Gly	Val	Asn	195	200	205	
Asn	Asn	Glu	Thr	Cys	Arg	His	Leu	Ser	Cys	Val	Leu	Ser	Gly	Leu	Ile	210	215	220	
Ala	Asp	Leu	Asp	Ala	Leu	Asp	Val	Cys	Gly	Arg	Thr	Glu	Ile	Arg	Asn	225	230	235	240
Tyr	Arg	Arg	Glu	Val	Val	Glu	Asp	Ile	Asn	Lys	Leu	Leu	Lys	Tyr	Leu	245	250	255	
Asp	Leu	Glu	Glu	Glu	Ala	Asp	Thr	Thr	Lys	Ala	Phe	Asp	Leu	Arg	Gln	260	265	270	
Asn	His	Ser	Ile	Leu	Lys	Ile	Glu	Lys	Val	Leu	Lys	Arg	Met	Arg	Glu	275	280	285	
Ile	Lys	Asn	Glu	Leu	Leu	Gln	Ala	Gln	Asn	Pro	Ser	Glu	Leu	Tyr	Leu	290	295	300	
Ser	Ser	Lys	Thr	Glu	Leu	Gln	Gly	Leu	Ile	Gly	Gln	Leu	Asp	Glu	Val	305	310	315	320
Ser	Leu	Glu	Lys	Asn	Pro	Cys	Ile	Arg	Glu	Ala	Arg	Arg	Arg	Ala	Val	325	330	335	
Ile	Glu	Val	Gln	Thr	Leu	Ile	Thr	Tyr	Ile	Asp	Leu	Lys	Glu	Ala	Leu	340	345	350	
Glu	Lys	Arg	Lys	Leu	Phe	Ala	Cys	Glu	Glu	His	Pro	Ser	His	Lys	Ala	355	360	365	
Val	Trp	Asn	Val	Leu	Gly	Asn	Leu	Ser	Glu	Ile	Gln	Gly	Glu	Val	Leu	370	375	380	

Ser Phe Asp Gly Asn Arg Thr Asp Lys Asn Tyr Ile Arg Leu Glu Glu  
385 390 395 400

Leu Leu Thr Lys Gln Leu Leu Ala Leu Asp Ala Val Asp Pro Gln Gly  
405 410 415

Glu Glu Lys Cys Lys Ala Ala Arg Lys Gln Ala Val Arg Leu Ala Gln  
420 425 430

Asn Ile Leu Ser Tyr Leu Asp Leu Lys Ser Asp Glu Trp Glu Tyr  
435 440 445